

FIG. 1

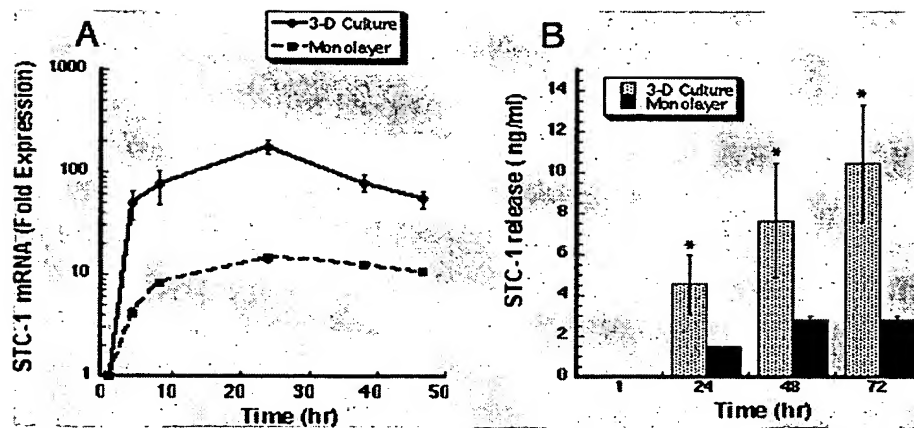


FIG. 2

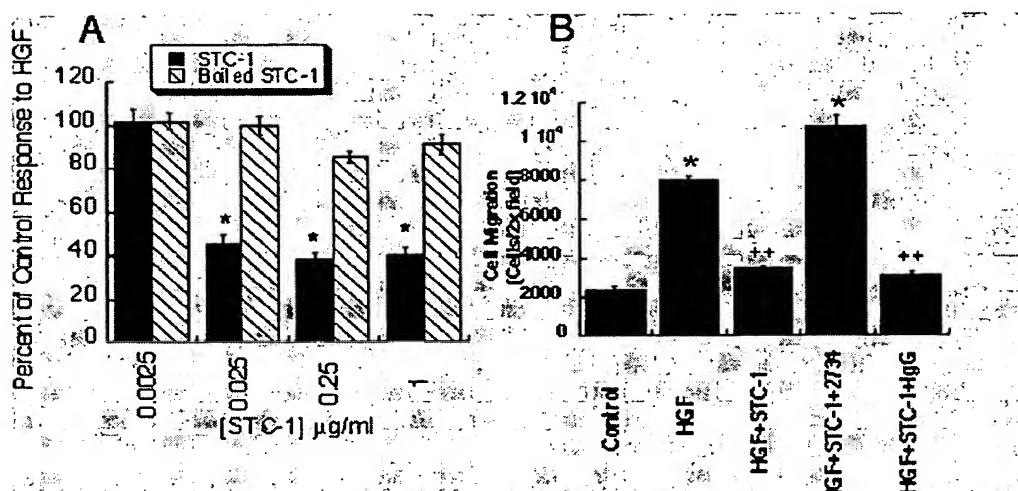


FIG. 3

A

B

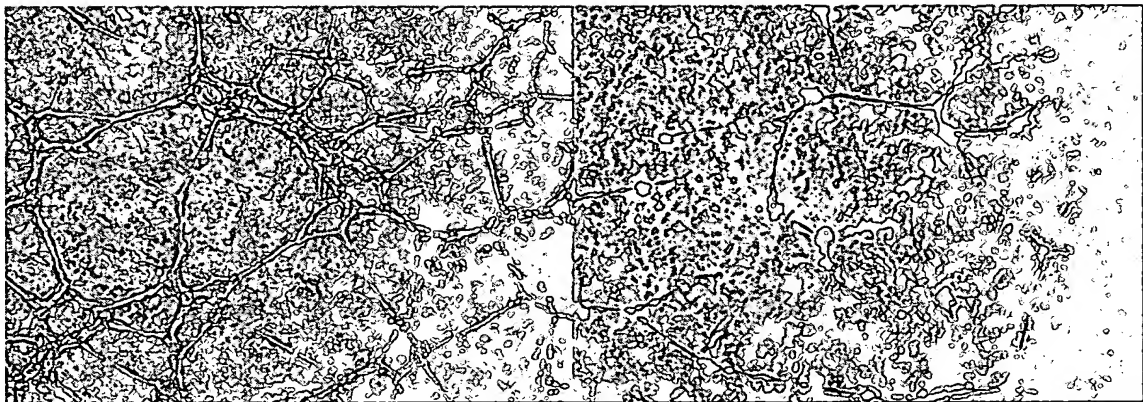
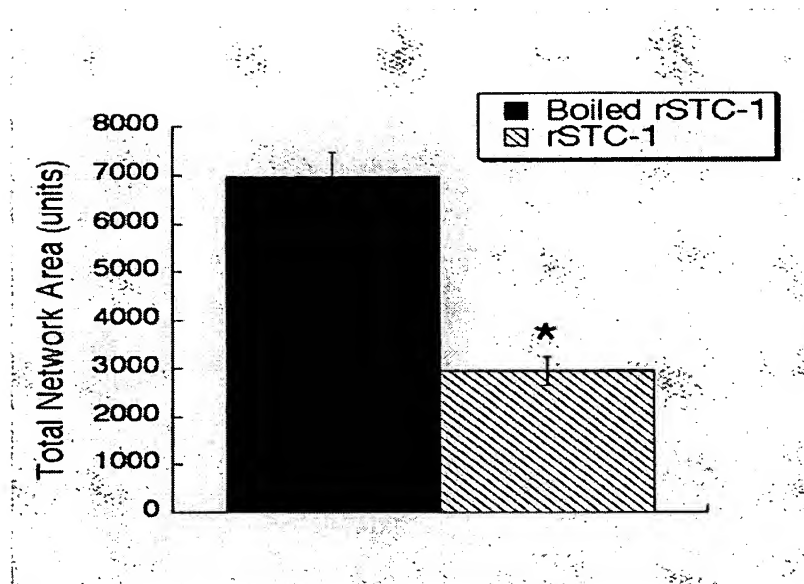


FIG. 3C



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FIG. 4

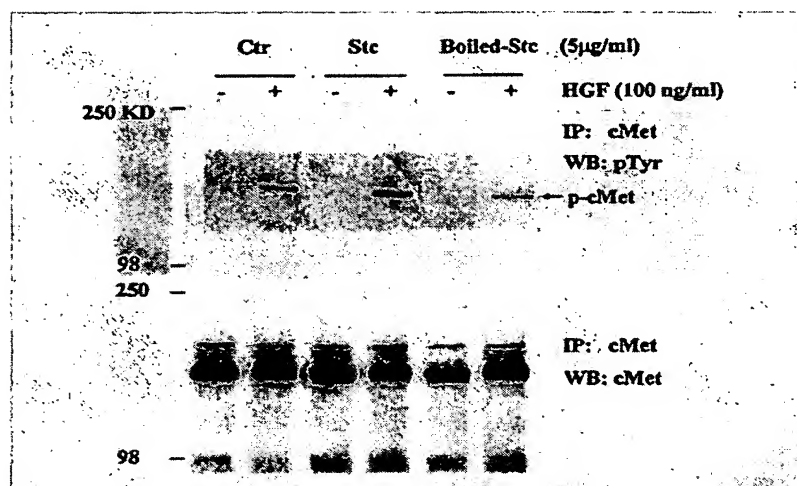


FIG. 5

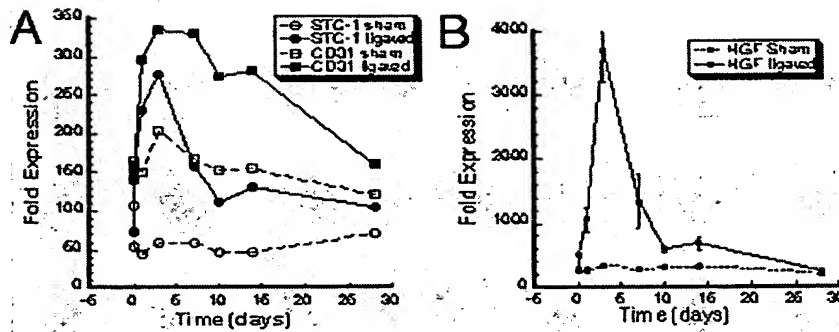


FIG. 6A

CAGTTTGCAAAAGCCAGAGGTGCAAGAAGCAGCGACTGCAGCAGCAGCAGCAGCAGCAGCGGC
GGTGGCAGCAGCAGCAGCAGCAGCGGCGGCAGCAGCAGCAGCAGCAGCGGAGGCACCGGTGGCAGC
AGCAGCATCACCAGCAACAACAACAAAAAAATCCTCATCAAATCCTCACCTAAGCTTT
CAGTGTATCCAGATCCACATCTTCACTCAAGCCAGGAGAGGGAAAGAGGAAAGGGGGGCA
GGAAAAAACCACAACTTAGCGGAACTTCTCAGAGAATGCTCCAAACTCAG
CAGTGCTTCTGGTGCTGGTGATCAGTGCTTCTGCAACCCATGAGGCGGAGCAGAATGACT
CTGTGAGCCCCAGGAAATCCCGAGTGGCGGCTCAAACTCAGCTGAAGTGGTTCGTTGCC
TCAACAGTGCTCTACAGGTCGGCTGCGGGGCTTTTGATGCCTGGAAAACCTCACCTGTG
ACACAGATGGGATGTATGACATCTGTAAATCCTTCTGTACAGCGCTGCTAAATTTGACA
CTCAGGGAAAAGCATTCGTCAAAGAGAGCTTAAAATGCATCGCCAACGGGGTCACCTCCA
AGGTCTTCCTCGCCATTCGGAGGTGCTCCACTTTCCAAAGGATGATTGCTGAGGTGCAGG
AAGAGTGCTACAGCAAGCTGAATGTGTGCAGCATCGCCAAGCGGAACCTGAAGCCATCA
CTGAGGTGCTCAGCTGCCAATCACTTCTCCAACAGATACTATAACAGACTTGTCCGAA
GCCTGCTGGAATGTGATGAAGACACAGTCAGCACAAATCAGAGACAGCCTGATGGAGAAAA
TTGGGCCTAACATGGCCAGCCTCTCCACATCCTGCAGACAGACCACTGTGCCCAAACAC
ACCCACGAGCTGACTTCAACAGGAGACGCACCAATGAGCCGCAGAAGCTGAAAGTCCTCC
TCAGGAACCTCCGAGGTGAGGAGGACTCTCCCTCCACATCAAACGCACATCCCATGAGA
GTGCATAACCAGGGAGAGGTTATTCAACCTCACCAAACCTAGTATCATTTTAGGGGTGT
TGACACACCAATTTTGAGTGTACTGTGCCTGGTTTGATTTTTTTAAAGTAGTTCCTATTT
TCTATCCCCCTTAAAGAAAATTGCATGAAACTAGGCTTCTGTAATCAATATCCCAACATT
CTGCAATGGCAGCATTCACCAACAAAATCCATGTGATCATTCTGCCTCTCCTCAGGAG
AAAGTACCTCTTTTACCAACTTCCTCTGCCATGTCTTTTCCCTGCTCCCTGAGACCA
CCCCAAACACAAAACATTCATGTAACCTCTCCAGCCATTGTAATTTGAAGATGTGGATCC
CTTTAGAACGGTTGCCCCAGTAGAGTTAGCTGATAAGGAACTTTATTTAAATGCATGTC
TTAAATGCTCATAAAGATGTTAAATGGAATTCGTGTTATGAATCTGTGCTGGCCATGGAC
GAATATGAATGTCACATTTGAATCTTGATCTCTAATGAGCTAGTGCTTATGGTCTTGA
TCCTCCAATGTCTAATTTTCTTTCCGACACATTTACCAAATTGCTTGAGCCTGGCTGTCC
AACCAGACTTTGAGCCTGCATCTTCTTGATCTAATGAAAAACAAAAAGCTAACATCTTT

FIG. 6B

ACGTACTGTAAGTCTCAGAGCTTTAAAAGTATCTTTAACAATTGTCTTAAAACCAGAGA
ATCTTAAGGTCTAACTGTGGAATATAAATAGCTGAAAATAATGTACTGTACATAAATTC
CAGAGGACTCTGCTTAAACAAAGCAGTATATAATAACTTTATTGCATATAGATTTAGTTT
TGTAAGTTAGCTTTATTTTCTTTTCTGGGAATGGAATAACTATCTCACTTCCAGATAT
CCACATAAATGCTCCTTGTGGCCTTTTTTATACTAAGGGGGTAGAAGTAGTTTAAATTC
AACATCAAACTTAAGATGGGCCTGTATGAGACAGGAAAAACCAACAGGTTTATCTGAAG
GACCCAGGTAAGATGTTAATCTCCAGCCACCTCAACCCAGAGGCTACTCTTGACTTA
GACCTATACTGAAAGATCTCTGTCACATCCAAGTGGAAATTCAGGAACCAAAAAGAGCA
TCCCTATGGGCTTGACCCTTACAGTGTGATAAGGCCTACTATACATTAGGAAGTGGTA
GTTCTTTACTCGTCCCCTTTCATCGGTGCCTGGTACTCTGGCAAATGATGATGGGGTGGG
AGACTTTCCATTAAATCAATCAGGAATGAGTCAATCAGCCTTTAGGTCTTTAGTCCGGGG
GACTTGGGGCTGAGAGAGTATAAATAACCTGGGCTGTCCAGCCTTAATAGACTTCTCTT
ACATTTTCGTCTGTAGCACGCTGCCTGCCAAAGTAGTCTTGGCAGCTGGACCATCTCTG
TAGGATCGTAAAAAATAGAAAAAAGAAAAAAGAAAGAAAGAGGGAAAAAGAGCT
GGTGGTTTGATCATTTCTGCCATGATGTTTACAAGATGGCGACCACCAAAGTCAAACGAC
TAACCTATCTATGAACAACAGTAGTTTCTCAGGGTCACTGTCTTGAACCCAACAGTCCC
TTATGAGCGTCACTGCCCACCAAAGGTCAATGTCAAGAGAGGAAGAGAGGGAGGAGGGGT
AGGACTGCAGGGGCCACTCCAACTCGCTTAGGTAGAACTATTGGTGCTCGACTCTCAC
TAGGCTAACTCAAGATTTGACCAAATCGAGTGATAGGGATCCTGGTGGGAGGAGAGAGG
GCACATCTCCAGAAAAATGAAAAGCAATACAACCTTTACCATAAAGCCTTTAAAACCAGTA
ACGTGCTGCTCAAGGACCAAGAGCAATTGCAGCAGACCCAGCAGCAGCAGCAGCAGCACA
AACATTGCTGCCTTTGTCCCCACACAGCCTCTAAGCGTGCTGACATCAGATTGTTAAGGG
CATTTTTATACTCAGAACTGTCCCATCCCCAGGTCCCCAACTTATGGACACTGCCTTAG
CCTCTTGAAAATCAGGTAGACCATATTCTAAGTTAGACTCTTCCCCTCCCTCCCACACTT
CCCACCCCAGGCAAGGCTGACTTCTCTGAATCAGAAAAGCTATTAAAGTTTGTGTGTTG

FIG. 6C

TGTCCATTTTGCAAACCCAACTAAGCCAGGACCCCAATGCGACAAGTAGTTCATGAGTAT
TCCTAGCAAATTTCTCTCTTTCTTCAGTTCAGTAGATTTCTTTTTTCTTTTCTTTTTTT
TTTTTTTTTTTTTTTTTGGCTGTGACCTCTTCAAACCGTGGTACCCCCCTTTTCTCCCCAC
GATGATATCTATATATGTATCTACAATACATATATCTACACATACAGAAAGAAGCAGTTC
TCACATGTTGCTAGTTTTTTTGCTTCTCTTTCCCCCACCCTACTCCCTCCAATTCCCCCT
TAAACTTCCAAAGCTTCGTCTTGTGTTTGTCTGCAGAGTGATTCTGGGGGCTGACCTAGACC
AGTTTGCATGATTCTTCTCTTGTGATTGGTTGCACTTTAGACATTTTTTGTGCCATTATA
TTTGCATTATGTATTTATAATTTAAATGATATTTAGGTTTTTGGCTGAGTACTGGAATAA
ACAGTGAGCATATCTGGTATATGTCATTATTTATTGTTAAATTACATTTTTTAAAGCTCCA
TGTGCATATAAAGGTTATGAAACATATCATGGTAATGACAGATGCAAGTTATTTTATTTG
CTTATTTTTTATAATTAAAGATGCCATAGCATAATATGAAGCCTTTGGTGAATTCCTTCT
AAGATAAAAATAATAATAAAGTGTTACGTTTTATTGGTTTCAAAAAAAAAAAAAAAAAAAAA
A (SEQ ID NO:1)

MLQNSAVLLVLVISASATHEAEQNDVSPRKSRVAAQNSAEVVRCNLNSALQVCGAFACL
ENSTCDTDGMYDICKSFLYSAAKFDTQGKAFVKESLKCIANGVTSKVFLAIRRCSTFORM
IAEVQEECYSKLNVCSIAKRNPEAITEVVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD
SLMEKIGPNMASLFHILQTDHCAQTHPRADFNRRRTNEPQKLKVLLRNLRGEEDSPSHIK
RTSHESA (SEQ ID NO:2)